

SEQUENCE LISTING

<110> Cowsert, Lex M.

Baker, Brenda F.

McNeil, John

Freier, Susan M.

Sasmor, Henri M.

Brooks, Douglas G.

Ohashi, Cara

Wyatt, Jacqueline R.

Borchers, Alexander

Vickers, Timothy A.

<120> Identification of Genetic Targets for Modulation by
Oligonucleotides and Generation of Oligonucleotides for Gene
Modulation

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Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe
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95 100 105

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 Arg Gly Cys Pro Ile Leu
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 Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp
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 Lys Ala Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe
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 Ser Glu His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln
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 275 280 285

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 Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
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Leu Ile Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe
495 500 505 510

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ccccgccccc ccggagctgc caacattgcc aacgccaccg ccacgctaca cacagcctca 180

actttcagga gaccgcctcg tggccttatt tattccaccc ttctgtaca tcgtagcgaa 240

tcaatccgtg gcgccgcact cctccgcac cctctttaac agtaccctg ggatggcgtg 300

agcactcccc cagcg atg gac cca tct gtg acg ctg tgg cag ttt ctg 348

Met Asp Pro Ser Val Thr Leu Trp Gln Phe Leu

1 5 10

ctg cag ctg ctg aga gag caa ggc aat ggc cac atc atc tcc tgg act 396

Leu Gln Leu Leu Arg Glu Gln Gly Asn Gly His Ile Ile Ser Trp Thr

15 20 25

tca cgg gat ggt ggt gaa ttc aag ctg gtg gat gca gag gag gtg gcc 444
Ser Arg Asp Gly Gly Glu Phe Lys Leu Val Asp Ala Glu Glu Val Ala
30 35 40

cgg ctg tgg gga cta cgc aag aac aag acc aac atg aat tac gac aag 492
Arg Leu Trp Gly Leu Arg Lys Asn Lys Thr Asn Met Asn Tyr Asp Lys
45 50 55

ctc agc cgg gcc ttg cgg tac tac tat gac aag aac atc atc cgc aag 540
Leu Ser Arg Ala Leu Arg Tyr Tyr Asp Lys Asn Ile Ile Arg Lys
60 65 70 75

gtg agc ggc cag aag ttc gtc tac aag ttt gtg tcc tac cct gag gtc 588
Val Ser Gly Gln Lys Phe Val Tyr Lys Phe Val Ser Tyr Pro Glu Val
80 85 90

gca ggg tgc tcc act gag gac tgc ccg ccc cag cca gag gtg tct gtt 636
Ala Gly Cys Ser Thr Glu Asp Cys Pro Pro Gln Pro Glu Val Ser Val
95 100 105

acc tcc acc atg cca aat gtg gcc cct gct gct ata cat gcc gcc cca 684
Thr Ser Thr Met Pro Asn Val Ala Pro Ala Ala Ile His Ala Ala Pro
110 115 120

ggg gac act gtc tct gga aag cca ggc aca ccc aag ggt gca gga atg 732
Gly Asp Thr Val Ser Gly Lys Pro Gly Thr Pro Lys Gly Ala Gly Met
125 130 135

gca ggc cca ggc ggt ttg gca cgc agc agc cgg aac gag tac atg cgc 780
Ala Gly Pro Gly Gly Leu Ala Arg Ser Ser Arg Asn Glu Tyr Met Arg
140 145 150 155

tcg ggc ctc tat tcc acc ttc acc atc cag tct ctg cag ccg cag cca 828
Ser Gly Leu Tyr Ser Thr Phe Thr Ile Gln Ser Leu Gln Pro Gln Pro
160 165 170

ccc cct cat cct cgg cct gct gtg gtg ctc ccc aat gca gct cct gca 876
Pro Pro His Pro Arg Pro Ala Val Leu Pro Asn Ala Ala Pro Ala
175 180 185

ggg gca gca gcg ccc ccc tcg ggg agc agg agc acc agt cca agc ccc 924
Gly Ala Ala Ala Pro Pro Ser Gly Ser Arg Ser Thr Ser Pro Ser Pro
190 195 200

ttg gag gcc tgt ctg gag gct gaa gag gcc ggc ttg cct ctg cag gtc 972
 Leu Glu Ala Cys Leu Glu Ala Glu Glu Ala Gly Leu Pro Leu Gln Val
 205 210 215

atc ctg acc ccg ccc gag gcc cca aac ctg aaa tcg gaa gag ctt aat 1020
 Ile Leu Thr Pro Pro Glu Ala Pro Asn Leu Lys Ser Glu Glu Leu Asn
 220 225 230 235

gtg gag ccg ggt ttg ggc cgg gct ttg ccc cca gaa gtg aaa gta gaa 1068
 Val Glu Pro Gly Leu Gly Arg Ala Leu Pro Pro Glu Val Lys Val Glu
 240 245 250

ggg ccc aag gaa gag ttg gaa gtt gcg ggg gag aga ggg ttt gtg cca 1116
 Gly Pro Lys Glu Glu Leu Glu Val Ala Gly Glu Arg Gly Phe Val Pro
 255 260 265

gaa acc acc aag gcc gag cca gaa gtc cct cca cag gag ggc gtg cca 1164
 Glu Thr Thr Lys Ala Glu Pro Glu Val Pro Pro Gln Glu Gly Val Pro
 270 275 280

gcc cgg ctg ccc gcg gtt gtt atg gac acc gca ggg cag gcg ggc ggc 1212
 Ala Arg Leu Pro Ala Val Val Met Asp Thr Ala Gly Gln Ala Gly Gly
 285 290 295

cat gcg gct tcc agc cct gag atc tcc cag ccg cag aag ggc cgg aag 1260
 His Ala Ala Ser Ser Pro Glu Ile Ser Gln Pro Gln Lys Gly Arg Lys
 300 305 310 315

ccc cgg gac cta gag ctt cca ctc agc ccg agc ctg cta ggt ggg ccg 1308
 Pro Arg Asp Leu Glu Leu Pro Leu Ser Pro Ser Leu Leu Gly Gly Pro
 320 325 330

gga ccc gaa cgg acc cca gga tcg gga agt ggc tcc ggc ctc cag gct 1356
 Gly Pro Glu Arg Thr Pro Gly Ser Gly Ser Gly Ser Gly Leu Gln Ala
 335 340 345

ccg ggg ccg gcg ctg acc cca tcc ctg ctt cct acg cat aca ttg acc 1404
 Pro Gly Pro Ala Leu Thr Pro Ser Leu Leu Pro Thr His Thr Leu Thr
 350 355 360

ccg gtg ctg ctg aca ccc agc tcg ctg cct cct agc att cac ttc tgg 1452
 Pro Val Leu Leu Thr Pro Ser Ser Leu Pro Pro Ser Ile His Phe Trp
 365 370 375

agc acc ctg agt ccc att gcg ccc cgt agc ccg gcc aag ctc tcc ttc 1500
 Ser Thr Leu Ser Pro Ile Ala Pro Arg Ser Pro Ala Lys Leu Ser Phe

380 385 390 395

cag ttt cca tcc agt ggc agc gcc cag gtg cac atc cct tct atc agc 1548
Gln Phe Pro Ser Ser Gly Ser Ala Gln Val His Ile Pro Ser Ile Ser
400 405 410

gtg gat ggc ctc tcg acc ccc gtg gtg ctc tcc cca ggg ccc cag aag 1596
Val Asp Gly Leu Ser Thr Pro Val Val Leu Ser Pro Gly Pro Gln Lys
415 420 425

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tggtggggtg gggatccttg ggaagaatta ctccaagag taactctcat tatctctcc 1772

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gggatgagcc tgacctaac ttttaggggtg gttaggacat ctccccacc tccccacttt 1952

tttccccaag acaagacaat cgaggtctgg ctgagaacg accttcttt ctttatttct 2012

cagcctgccc ttggggagat gagggagccc tgtctgcgtt ttggatgtg agtagaagag 2072

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atttaatggg ttgggagtct tggccaagga agaatcacac ccttggaata gaaatttcca 2192

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 Glu Ser Lys Arg Ile Asn Ala Glu Ile Glu Lys Gln Leu Arg Arg Asp
 20 25 30

aag cgc gac gcc cgg cgc gag ctc aag ctg ctg ctg ctc ggc acg ggc 144
 Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Gly Thr Gly
 35 40 45

gag agc ggg aag agc acg ttc atc aag cag atg cgc atc atc cac ggc 192
 Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
 50 55 60

gcc ggc tac tcg gag gag gac aag cgc ggc ttc acc aag ctc gtc tac 240
 Ala Gly Tyr Ser Glu Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
 65 70 75 80

cag aac atc ttc acc gcc atg cag gcc atg atc cgg gcc atg gag acg 288
 Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Glu Thr
 85 90 95

ctc aag atc ctc tac aag tac gag cag aac aag gcc aat gcg ctc ctg 336
 Leu Lys Ile Leu Tyr Lys Tyr Glu Gln Asn Lys Ala Asn Ala Leu Leu
 100 105 110

atc cgg gag gtg gac gtg gag aag gtg acc acc ttc gag cat cag tac 384
 Ile Arg Glu Val Asp Val Glu Lys Val Thr Thr Phe Glu His Gln Tyr
 115 120 125

gtc agt gcc atc aag acc ctg tgg gag gac ccg ggc atc cag gaa tgc 432
 Val Ser Ala Ile Lys Thr Leu Trp Glu Asp Pro Gly Ile Gln Glu Cys
 130 135 140

tac gac cgc agg cgc gag tac cag ctc tcc gac tct gcc aag tac tac 480
Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr
145 150 155 160

ctg acc gac gtt gac cgc atc gcc acc ttg ggc tac ctg ccc acc cag 528
Leu Thr Asp Val Asp Arg Ile Ala Thr Leu Gly Tyr Leu Pro Thr Gln
165 170 175

cag gac gtg ctg cgg gtc cgc gtg ccc acc acc ggc atc atc gag tac 576
Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr
180 185 190

cct ttc gac ctg gag aac atc atc ttc cgg atg gtg gat gtg ggg ggc 624
Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly
195 200 205

cag cgg tcg gag cgg agg aag tgg atc cac tgc ttt gag aac gtg aca 672
Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr
210 215 220

tcc atc atg ttt ctc gtc gcc ctc agc gaa tac gac caa gtc ctg gtg 720
Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val
225 230 235 240

gag tcg gac aac gag aac cgg atg gag gag agc aaa gcc ctg ttc cgg 768
Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg
245 250 255

acc atc atc acc tac ccc tgg ttc cag aac tcc tcc gtc atc ctc ttc 816
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260 265 270

ctc aac aag aag gac ctg ctg gag gac aag atc ctg tac tcg cac ctg 864
Leu Asn Lys Lys Asp Leu Leu Glu Asp Lys Ile Leu Tyr Ser His Leu
275 280 285

gtg gac tac ttc ccc gag ttc gat ggt ccc cag cgg gac gcc cag gcg 912
Val Asp Tyr Phe Pro Glu Phe Asp Gly Pro Gln Arg Asp Ala Gln Ala
290 295 300

gcg cgg gag ttc atc ccg aag atg ttc gtg gac ctg aac ccc gac agc 960
Ala Arg Glu Phe Ile Pro Lys Met Phe Val Asp Leu Asn Pro Asp Ser
305 310 315 320

gac aag atc atc tac tca cac ttc acg tgt gcc acc gac acg gag aac 1008
Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn

325 330 335
 atc cgc ttc gtg ttc gcg gcc gtg aag gac acc atc ctg cag ctg aac 1056
 Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn
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